

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5
- (i) APPLICANT: Glimcher, Laurie H. et al.
- (ii) TITLE OF INVENTION: Human c-Maf Compositions and  
Methods of Use Thereof
- 10
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: LAHIVE & COCKFIELD, LLP  
(B) STREET: 28 State Street  
(C) CITY: Boston  
(D) STATE: Massachusetts  
(E) COUNTRY: USA  
(F) ZIP: 02109
- 20
- (v) COMPUTER READABLE FORM:
- 25 (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
- 30 (A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- 35 (A) APPLICATION NUMBER: 09/030,579  
(B) FILING DATE: 2-FEB-1998
- (viii) ATTORNEY/AGENT INFORMATION:
- 40 (A) NAME: Kara, Catherine J.  
(B) REGISTRATION NUMBER: 41,106  
(C) REFERENCE/DOCKET NUMBER: HUI-027CP
- (ix) TELECOMMUNICATION INFORMATION:
- 45 (A) TELEPHONE: (617) 227-7400  
(B) TELEFAX: (617) 742-4214

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 1203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- 55
- (ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..1203

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCA TCA GAA CTG GCA ATG AGC AAC TCC GAC CTG CCC ACC AGT CCC  
48  
Met Ala Ser Glu Leu Ala Met Ser Asn Ser Asp Leu Pro Thr Ser Pro  
10 1 5 10 15  
CTG GCC ATG GAA TAT GTT AAT GAC TTC GAT CTG ATG AAG TTT GAA GTG  
96  
Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val  
15 20 25 30  
AAA AAG GAA CCG GTG GAG ACC GAC CGC ATC ATC AGC CAG TGC GGC CGT  
144  
Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg  
20 35 40 45  
CTC ATC GCC GGG GGC TCG CTG TCC TCC ACC CCC ATG AGC ACG CCC TGC  
192  
Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys  
25 50 55 60  
AGC TCG GTG CCC CCG TCC CCC AGC TTC TCG GCG CCC AGC CCG GGC TCG  
240  
Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser  
30 65 70 75 80  
CGA GGC GAA CAG AAG GCG CAC CTG GAA GAC TAC TAC TGG ATG ACC GGC  
288  
Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly  
35 85 90 95  
TAC CCG CAG CAG CTG AAC CCC GAG GCG CTG GGC TTC AGC CCC GAG GAC  
336  
Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp  
40 100 105 110  
GCG GTC GAG GCG CTC ATC AGC AAC AGC CAC CAG CTC CGG GGC GGC TTC  
384  
Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe  
45 115 120 125  
GAT GGC TAT GCG CGC GGG GCG CAG CAG CTA GCC GCG GCG GCC GGG GCA  
432  
Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Ala Gly Ala  
50 130 135 140  
GGT GCC GGC GCC TCC TTG GGC GGC AGC GGC GAG GAG ATG GGC CCC GCC  
480  
Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala  
55 145 150 155 160

GCC GCC GTG GTG TCC GCC GTG ATC GCC GCG GCC GCC GCG CAG AGC GGC  
 528  
 Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Ala Gln Ser Gly  
 165 170 175  
 5  
 GCG GGC CCG CAC TAC CAC CAC CAC CAC CAC CAC GCC GCC GGC CAC CAC  
 576  
 Ala Gly Pro His Tyr His His His His His His Ala Ala Gly His His  
 180 185 190  
 10  
 CAC CAC CCG ACG GCC GGC GCG CCC GGC GCC GCG GGC AGC GCG GCC GCT  
 624  
 His His Pro Thr Ala Gly Ala Pro Gly Ala Ala Gly Ser Ala Ala Ala  
 195 200 205  
 15  
 TCG GCC GGT GGC GCT GGG GGC GCG GGC GGC GGT GGC CCG GCC AGC GTT  
 672  
 Ser Ala Gly Gly Ala Gly Gly Ala Gly Gly Gly Gly Pro Ala Ser Val  
 210 215 220  
 20  
 GGG GGC GGC GGC GGC GGC GGC GGC GGC GGA GGC GGC GGG GGC GCG GCG  
 720  
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala  
 225 230 235 240  
 25  
 GGC GCC CTG CAC CCG CAC CAC GCC GCC GGC GGC CTG CAC TTC GAC GAC  
 768  
 Gly Ala Leu His Pro His His Ala Ala Gly Gly Leu His Phe Asp Asp  
 245 250 255  
 30  
 CGC TTC TCC GAC GAG CAG CTG GTG ACC ATG TCT GTG CGC GAC TGG AAC  
 816  
 Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Asp Trp Asn  
 260 265 270  
 35  
 CGG CAG CTG CGC GGG GTC AGC AAG GAG GAG GTG ATC CGG CTG AAG CAG  
 864  
 Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln  
 275 280 285  
 40  
 AAG AGG CGG ACC CTG AAA AAC CGC GGC TAT GCC AAG TCC TGC CGC TTC  
 912  
 Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe  
 290 295 300  
 45  
 AAG AGG GTG CAG CAG AGA CAC GTC CTG GAG TCG GAG AAG AAC CAG CTG  
 960  
 Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu  
 305 310 315 320  
 50  
 CTG CAG CAA GTC GAC CAC CTC AAG CAG GAG ATC TCC AGG CTG GTG CGC  
 1008  
 Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg  
 325 330 335  
 55  
 GAG AGG GAC GCG TAC AAG GAG AAA TAC GAG AAG TTG GTG AGC AGC GGC  
 1056

1000  
 900  
 800  
 700  
 600  
 500  
 400  
 300  
 200  
 100  
 0

Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly  
340 345 350

5 TTC CGA GAA AAC GGC TCG AGC AGC GAC AAC CCG TCC TCT CCC GAG TTT  
1104

Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe  
355 360 365

10 TTC ATA ACT GAG CCC ACT CGC AAG TTG GAG CCA TCA GTG GGA TAC GCC  
1152

Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala  
370 375 380

15 ACA TTT TGG AAG CCC CAG CAT CGT GTA CTT ACC AGT GTG TTC ACA AAA  
1200

Thr Phe Trp Lys Pro Gln His Arg Val Leu Thr Ser Val Phe Thr Lys  
385 390 395 400

20 TGA  
1203

25 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 amino acids

(B) TYPE: amino acid

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

35 Met Ala Ser Glu Leu Ala Met Ser Asn Ser Asp Leu Pro Thr Ser Pro  
1 5 10 15

40 Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val  
20 25 30

Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg  
35 40 45

45 Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys  
50 55 60

Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser  
65 70 75 80

5 Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly  
85 90 95

55 Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp  
100 105 110

Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe

	115	120	125
	Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Ala Gly Ala		
	130	135	140
5	Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala		
	145	150	155
	Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Ala Gln Ser Gly		
10		165	170
	Ala Gly Pro His Tyr His His His His His His Ala Ala Gly His His		
	180	185	190
15	His His Pro Thr Ala Gly Ala Pro Gly Ala Ala Gly Ser Ala Ala Ala		
	195	200	205
	Ser Ala Gly Gly Ala Gly Gly Ala Gly Gly Gly Gly Pro Ala Ser Val		
20	210	215	220
	Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala		
	225	230	235
	Gly Ala Leu His Pro His His Ala Ala Gly Gly Leu His Phe Asp Asp		
25		245	250
	Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Asp Trp Asn		
	260	265	270
30	Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln		
	275	280	285
	Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe		
35	290	295	300
	Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu		
	305	310	315
	Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg		
40		325	330
	Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly		
	340	345	350
45	Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe		
	355	360	365
	Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala		
50		375	380
	Thr Phe Trp Lys Pro Gln His Arg Val Leu Thr Ser Val Phe Thr Lys		
	385	390	395
			400

115 120 125